Genome-wide approaches to dissect the roles of RNA binding proteins in translational control: implications for neurological diseases.

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Public Summary:
Translational control of messenger RNAs (mRNAs) is a key aspect of neurobiology, defects of which can lead to neurological diseases. In response to stimuli, local translation of mRNAs is activated at synapses to facilitate long-lasting forms of synaptic plasticity, the cellular basis for learning, and memory formation. Translation, as well as all other aspects of RNA metabolism, is controlled in part by RNA binding proteins (RBPs) that directly interact with mRNAs to form mRNA-protein complexes. Disruption of RBP function is becoming widely recognized as a major cause of neurological diseases. Thus understanding the mechanisms that govern the interplay between translation control and RBP regulation in both normal and diseased neurons will provide new opportunities for novel diagnostics and therapeutic intervention. As a means of studying translational control, genome-wide methods are emerging as powerful tools that have already begun to unveil mechanisms that are missed by single-gene studies. Here, we describe the roles of RBPs in translational control, review genome-wide approaches to examine translational control, and discuss how the application of these approaches may provide mechanistic insight into the pathogenic underpinnings of RBPs in neurological diseases.

Scientific Abstract:
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